

Does Magnesium Transport Protein (MgtE) Contribute to the Antibiotic Resistance of *Pseudomonas aeruginosa*?

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Pseudomonas aeruginosa is an environmental and opportunistic bacterial pathogen that is resistant to antibiotic treatment when it forms biofilms in the lungs of patients with cystic fibrosis. Biofilms are densely packed communities of bacteria embedded within a self-produced matrix of extracellular polymeric substance (EPS). Biofilm EPS is a polymeric cluster composed of extracellular DNA, proteins and polysaccharides. Based on previous studies, in a low Mg^{2+} environment, *P. aeruginosa* wild-type is less or non-resistant to antibiotics and in a high Mg^{2+} environment, *P. aeruginosa* is more resistant to antibiotics. The purpose of this project was to find out if the magnesium transport protein (MgtE) is a contributor to the antibiotic resistance of *P. aeruginosa*. This was accomplished by using two different strains of *P. aeruginosa*; PA14 wild-type and GGA52 mutant (without the magnesium transporting protein). Four antibiotics were used; gentamicin, tobramycin, ciproflaxin and imipenem. The minimum inhibitory concentration (MIC) of each antibiotic was determined by culturing the bacteria strains on LB agar plates and use Etest strips to observe growth. N-minimal media supplemented with varying magnesium concentration was used to test if Mg^{2+} increased or reduced the antibiotic resistance at the MIC of *P. aeruginosa* as well as counting bacterial colonies. The mutant strain (GGA52) is expected to be less resistant than the wild type strain (PA14) because it does not have MgtE. If these predictions are true, then MgtE is an important contributor to the antibiotic resistance of *P. aeruginosa*. These results can be helpful in understanding the mechanism of antibiotic resistance of *P. aeruginosa* in patients with cystic fibrosis.

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